

REMARKS

In response to the Notice of Non-Compliant Amendment (37 C.F.R. 1.121) mailed July 23, 2001, please find enclosed an amendment which includes a clean version of the replacement paragraph and a marked-up version of the replacement paragraph.

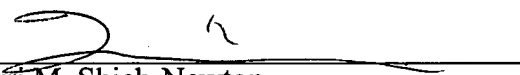
Attached hereto is a marked-up version of the changes made to the specification by the current amendment. The attached page is captioned **"Version with marking to show changes made."**

In the unlikely event that the transmittal letter is separated from this sequence listing and the U.S. Patent Office determines that an extension and/or other relief is required, Applicants petition for any required relief including extensions of time and authorize the Assistant Commissioner to charge the cost of such petitions and/or other fees due in connection with the filing of this sequence listing to our **Deposit Account No. 03-1952**. However, the Assistant Commissioner is not authorized to charge the cost of the issue fee to the Deposit Account.

Respectfully submitted,

Dated: August 2, 2001

By:


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VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the specification:

Panel A of Figure 6 depicts the complete DNA sequence and the deduced amino acid sequence (SEQ ID NOS:3-4) of Ag 2160. The nucleotide numbering is shown on the right and amino acid numbering is shown on the left of the sequence. The predicted sequence reveals a possible signal peptide (black overline), 2 potential N-linked glycosylation sites (gray overline), and a single 23-amino acid transmembrane domain (gray frame). Panel B is a Kyte-Doolittle plot of the deduced amino acid sequence. The predicted start and stop codons are also indicated. The putative hydrophobic signal peptide as well as the hydrophobic transmembrane domain are underlined. Panel C is a sequence alignment of Ag 2160 homologues that include mEGP, hEGP-2, hEGP-1 (SEQ ID NOS:5-8). The hydrophobic signal peptide and the hydrophobic transmembrane domain are underlined. The protein sequences are aligned with the type I thyroglobulin sequence repeat (framed). Conserved cysteine residues are in bold type while highly conserved regions are indicated. Panel D is a Northern blot showing the tissue distribution of the Ag 2160 mRNA.

Figure 10 depicts a partial cDNA clone of Ag 2117 (SEQ ID NOS:1-2) that is recognized by Mab 2117.